

Functional Data

Monday 1pm

Scan (session=4, scan_idx=7)

Field:field=1

ScanUnit:unit_id=1, mask_id=1

ScanUnit:unit_id=2, mask_id=2

:

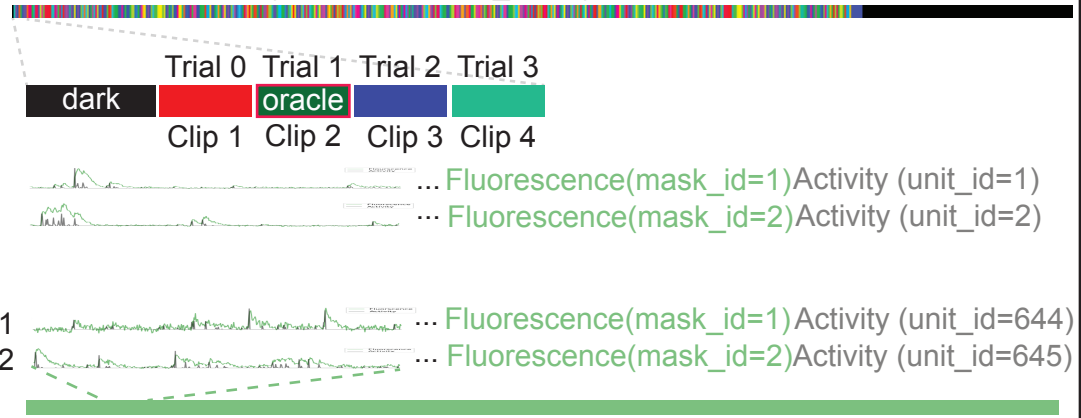
Field:field=2

ScanUnit:unit_id=644, mask_id=1

ScanUnit:unit_id=645, mask_id=2

:

Stimulus (session=4, scan_idx=7)



Tuesday 3pm

Scan (session=5, scan_idx=6)

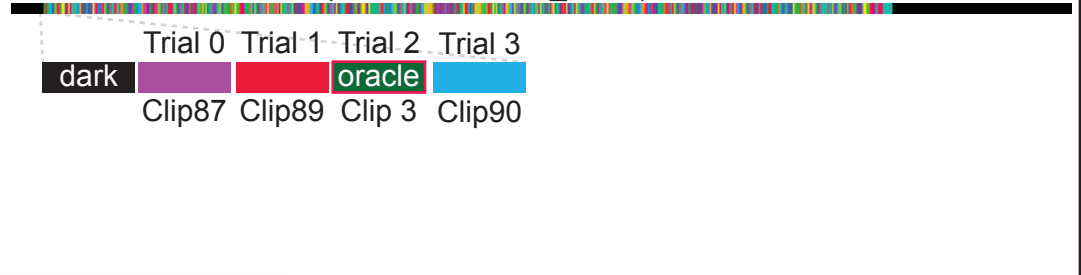
Field: field=1

ScanUnit:unit_id=1, mask_id=1

ScanUnit:unit_id=2, mask_id=2

:

Stimulus (session=5, scan_idx=6)



Imaging data structure

nda.Scan: Scans are collections of frames that were acquired simultaneously. They are defined by a combination of session and scan index. Information on completed scans. Cajal Pipeline: [meso.ScanInfo](#)

nda.ScanInclude: Scans determined suitable for analysis. Some scans did not complete successfully or had incomplete data, and so are not recommended.

nda.Field: Individual fields of scans. Fields are single image planes. Each scans contains 8 fields. See [here](#) for a visualization of the scans to understand how the fields are distributed Cajal Pipeline: [meso.ScanInfo.Field](#). On each frame of the scan, the microscope scanned one field, then hopped to the next field, and so on in a loop. So the individual 8 frames are spread out across the inter-scan frame time. All 8 frames were imaged within the 6.3Hz acquisition rate.

Timing and stimulus

nda.FrameTimes: Timestamps of scan frames in seconds relative to the start of the scan for the first pixel of the first imaging field. You can use this to get a precise timing of each unit in a consistent timebase.

nda.Stimulus: For each scan, contains the movie aligned to activity traces in `nda.Activity`. Note, this movie is now temporally downsampled to match the acquisition rate of the activity, but **does NOT reflect the temporal properties of the stimulus** that was actually shown to the animal. You have to download the actual stimulus movie at 30Hz if you want precise temporarily correct information about the pixels shown to the mouse during the scan. (see below)

nda.Trial: Contains information for each trial of the movie in `nda.Stimulus`. There are three types of trials, `Clip`, `Monet2`, and `Trippy`. Each unique trial has its own `condition_hash`. To get detailed information for each trial stimulus, join each `condition_hash` according to its corresponding type in one of: `nda.Clip`, `nda.Monet2`, or `nda.Trippy`.

nda.Clip: Detailed information for movie clips.

nda.Monet2: Detailed information for the Monet2 stimulus.

nda.Trippy: Detailed information for the Trippy stimulus.

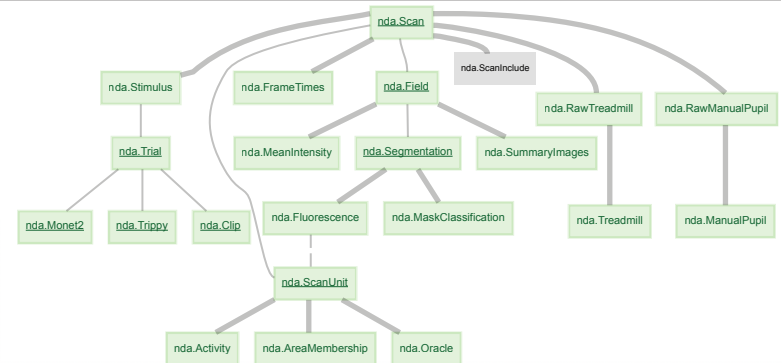
Behavior

nda.RawManualPupil: Pupil traces for each scan from the left eye collected at ~20 Hz and semi-automatically segmented.

nda.ManualPupil: Manual pupil traces low-pass filtered with a hamming window to the scan frame rate and linearly interpolated to scan frame times.

nda.RawTreadmill: Cylindrical treadmill rostral-caudal position extracted with a rotary optical encoder at ~100Hz and converted into velocity.

nda.Treadmill: Treadmill velocities low-pass filtered with a hamming window to the scan frame rate then linearly interpolated to scan frame times.



Functional extraction

nda.Segmentation: CNMF segmentation of a field using CalmAn package (<https://github.com/simonsfoundation/CalmAn>). It records the masks of all segmented cells. Mask_id's are unique per field. Cajal Pipeline: [meso.Segmentation.Mask](#)

nda.Fluorescence: Records the raw fluorescence traces for each segmented mask. Cajal Pipeline: [\[meso.Fluorescence.Trace\]](#) (<https://github.com/cajal/pipeline/blob/921a920478c73687dd78b863fcd05e12bbf1e197/python/pipeline/meso.py#L1159>)

nda.ScanUnit: Unit_id assignment that is unique across the entire scan. Includes info about each unit. Cajal Pipeline: [meso.ScanSet.Unit / meso.ScanSet.UnitInfo](#)

nda.Activity: Deconvolved spike trace from the fluorescence trace. Cajal Pipeline: [meso.Activity.Trace](#)

nda.MaskClassification: Classification of segmented masks into soma or artifact. Uses CalmAn package (<https://github.com/simonsfoundation/CalmAn>). Cajal Pipeline: [meso.MaskClassification.Type](#)

Functional analysis

nda.Oracle: Measures how reliably each ScanUnit responds to visual stimulus Leave-one-out correlation for repeated videos in stimulus.

nda.AreaMembership: Visual area labels for all units.

30Hz visual stimulus files

folder: https://bosssdb-open-data.s3.amazonaws.com/iarpa_microns/minnie/functional_data/stimulus_movies

filename_format: f'stimulus_17797_{session}_{scan_idx}_v1.avi'

Dataset Preprint:

Functional connectomics spanning multiple areas of mouse visual cortex. [nda docs](#):

bioRxiv 2021.07.28.454025; doi: <https://doi.org/10.1101/2021.07.28.454025> https://github.com/cajal/microns_phase3_nda